

REMARKS

The Examiner has required restriction of the claims, dividing them among 13 Groups as follows:

- I. Claims 1-10, 25, 26, 55 and 56, drawn to an isolated recombinant human metapneumovirus (rHMPV) comprising a partial or complete recombinant HMPV genome or antigenome comprising one or more attenuating nucleotide modification comprising a partial or complete deletion of a HMPV SH ORF such that a wild type SH protein is not produced, and a major nucleocapsid (N) protein, a nucleocapsid phosphoprotein (P) and a large polymerase protein (L), and an expression vector comprising the partial or complete rHMPV genome or antigenome under the control of a promoter, classified in class 424, subclasses 199.1 and 205.1.
- II. Claims 1-8, 11, 12, 25, 26, 55 and 56, drawn to an isolated recombinant human metapneumovirus (rHMPV) comprising a partial or complete recombinant HMPV genome or antigenome comprising one or more attenuating nucleotide medication comprising a partial or complete deletion of a HMPV G ORF such that a wild type G protein is not produced, and a major nucleocapsid (N) protein, a nucleocapsid phosphoprotein (P) and a large polymerase protein (L), and an expression vector comprising the partial or complete rHMPV genome or antigenome under the control of a promoter, classified in class 424, subclasses 199.1 and 205.1.
- III. Claims 1-8, 13, 14, 25, 26, 55 and 56, drawn to an isolated recombinant human metapneumovirus (rHMPV) comprising a partial or complete recombinant HMPV genome or antigenome comprising one or more attenuating nucleotide modification comprising a partial or complete deletion of a HMPV SH and G ORFs such that wild type SH and G proteins are not produced, and a major nucleocapsid (N) protein, a nucleocapsid phosphoprotein (P) and a large polymerase protein (L), and an

- expression vector comprising the partial or complete rHMPV genome or antigenome under the control of a promoter, classified in class 424, subclasses 199.1 and 205.1.
- IV. Claims 1-8, 15-19, 25, 26, 55 and 56, drawn to an isolated recombinant human metapneumovirus (rHMPV) comprising a partial or complete recombinant HMPV genome or antigenome comprising one or more attenuating nucleotide modification comprising one or more nucleotide substitution that reduces or ablates expression of rHMPV M2-2 ORF such that a wild type M2-2 protein is not produced, and a major nucleocapsid (N) protein, a nucleocapsid phosphoprotein (P) and a large polymerase protein (L), and an expression vector comprising the partial or complete rHMPV genome or antigenome under the control of a promoter, classified in class 424, subclasses 199.1 and 205.1.
- V. Claims 1-8, 20-22, 25-27, 55 and 56, drawn to an isolated recombinant human metapneumovirus (rHMPV) comprising a partial or complete recombinant HMPV genome or antigenome comprising one or more attenuating nucleotide modification comprising one or more nucleotide substitution that reduces or ablates expression of rHMPV M2-1 ORF such that a wild type M2-1 protein is not produced, and a major nucleocapsid (N) protein, a nucleocapsid phosphoprotein (P) and a large polymerase protein (L), and an expression vector comprising the partial or complete rHMPV genome or antigenome under the control of a promoter, classified in class 424, subclasses 199.1 and 205.1.
- VI. Claims 1-8, 23-26, 55 and 56, drawn to an isolated recombinant human metapneumovirus (rHMPV) comprising a partial or complete recombinant HMPV genome or antigenome comprising one or more attenuating nucleotide modification comprising a partial or complete deletion of a HMPV M2 ORF, and a major nucleocapsid (N) protein, a nucleocapsid phosphoprotein (P) and a large polymerase protein (L), and an expression vector comprising the partial or complete rHMPV genome or antigenome under the control of a promoter, classified in class 424, subclasses 199.1 and 205.1.

- VII. Claims 28-31, drawn to an isolated recombinant human metapneumovirus (rHMPV) comprising a partial or complete recombinant HMPV genome or antigenome, and a major nucleocapsid (N) protein, a nucleocapsid phosphoprotein (P) and a large polymerase protein (L), wherein the genome or antigenome is rearranged such that an order of one or more genes or genome segments is altered as compared to a wild type HMPV, and wherein a SH gene and a G gene or at least two copies of SH gene and at least two copies of G gene are inserted after a M gene and before a F gene, classified in class 424, subclasses 199.1 and 205.1.
- VIII. Claims 28, 29 and 32-35, drawn to an isolated recombinant human metapneumovirus (rHMPV) comprising a partial or complete recombinant HMPV genome or antigenome, and a major nucleocapsid (N) protein, a nucleocapsid phosphoprotein (P) and a large polymerase protein (L), wherein the genome or antigenome is rearranged such that an order of one or more genes or genome segments is altered as compared to a wild type HMPV, and wherein a F gene or a G gene or both a F gene and a G gene are inserted after a 3' leader sequence and before a N gene in the rHMPV genome or antigenome, classified in class 424, subclasses 199.1 and 205.1.
- IX. Claims 36-42, drawn to an isolated recombinant human metapneumovirus (rHMPV) comprising a partial or complete recombinant HMPV genome or antigenome, comprising one or more attenuating nucleotide modifications, and a major nucleocapsid (N) protein, a nucleocapsid phosphoprotein (P) and a large polymerase protein (L), wherein the one or more attenuating nucleotide modifications comprises inserting one or more additional copies of one or more rHMPV G or F genes or both after a 3' leader sequence and before a N gene in the rHMPV genome or antigenome, classified in class 424, subclasses 199.1 and 205.1.
- X. Claims 43-46, drawn to an isolated recombinant human metapneumovirus (rHMPV) comprising a partial or complete recombinant HMPV genome or antigenome, comprising one or more attenuating nucleotide modifications, and a major nucleocapsid (N) protein, a nucleocapsid phosphoprotein (P) and a large polymerase protein (L), wherein the rHMPV further comprises one or more heterologous genes or

- genome segments from a different paramyxovirus to form chimeric recombinant HMPV genome or antigenome, classified in class 424, subclasses 199.1 and 205.1.
- XI. Claims 47-51, drawn to an immunogenic composition comprising the isolated replication competent rHMPV of claim 1, and a method for inducing an immune response in a subject by administering to the subject said rHMPV, classified in class 424, subclass 93.1.
- XII. Claims 52-54, drawn to an isolated replication competent recombinant virus comprising a paramyxovirus genome or antigenome and a major nucleocapsid (N) protein, a nucleocapsid phosphoprotein (P) and a large polymerase protein (L), and one or more recombinant genes or genome segments for human metapneumovirus, classified in class 424, subclass 211.1.
- XIII. Claim 57, drawn to a method of screening an antiviral compound for inhibition of a biological activity of human metapneumovirus comprising providing a rHMPV comprising a major nucleocapsid (N) protein, a nucleocapsid phosphoprotein (P) and a large polymerase protein (L), and a partial or complete rHMPV genome or antigenome modified to incorporate a detectable heterologous sequence encoding a polypeptide correlated with the biological activity, exposing a sample to a test compound or a library of test compounds to determine inhibition of the biological activity of HMPV by said test compound(s), classified in class 435, subclass 5.

Applicants hereby elect for prosecution in this application the claims of Group IV, claims 1-8, 15-19, 25, 26, 55 and 56, with traverse.

Applicants submit that at least all of Groups I through VI should be recombined. Each of the various Groups I through IX sets forth a different species of attenuating mutation. Claim 1 is generic to the attenuating mutations recited in the various groups, as well-evidenced by inclusion of claim 1-8 in Groups I to VI. Applicants have no problem with the Examiner treating Groups I through VI in the manner of an election of species requirement, in which instance the species of "Group" II is elected for initial prosecution and the Examiner is invited to search further species

if the claims of “Group” II are found allowable, with an eye toward determining if the generic claim (1) is allowable. Applicants take note of the Examiner’s explanation that at least claim 1 is a linking claim.

Alternatively, Groups IV and VI should be rejoined. Applicants note that deletion is but a specific way to ablate expression of a gene.

Similarly, either or both of Groups I and II should be rejoined with Group III. Applicants note that the claims of both of these Groups are generic to the claims of Group III. Allowability of Group II especially establishes allowability of Group III.

Similarly, Groups IX and X should be rejoined. Allowability of the claims of Group IX will establish allowability of the claims of Group X.

Group XI, directed to a formulation and its use, should be rejoined, provided the claims are kept commensurate in scope with the otherwise elected Group of claims, upon a finding of allowable subject matter in the elected composition claims. Similarly, Group XIII represents a method of use of the elected composition and should be rejoined under similar conditions. MPEP 821.04.

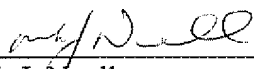
Should there be any outstanding matters that need to be resolved in the present application, the Examiner is respectfully requested to contact Dr. Mark Nuell, Registration No 36,623 at the telephone number of the undersigned below, to conduct an interview in an effort to expedite prosecution in connection with the present application.

- ☒ Attached is a Petition for Extension of Time.
- ☒ Attached hereto is the fee transmittal listing the required fees.

If necessary, the Commissioner is hereby authorized in this, concurrent, and future replies, to charge payment or credit any overpayment to our Deposit Account No. 02-2448 for any additional fees required under 37 C.F.R. § 1.16 or under § 1.17; particularly, extension of time fees.

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Respectfully submitted,

By 
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